

NRSEs present in neuronal genes			Intragenic Position
NRSEs present in neuronal genes	Consensus	Sequence	
CONSENSUS:	TTCAGCACCCnCGGAGAGnGCC		
SOG10	GCCAT	-----T-----	5' UTR
Na CHANNEL	TGGGT	-----A-----	5' UTR
SYNAPSIN I	CCAGC	-----C-----	5' UTR
BDNF	GTCCA	-----T-----	5' UTR
GLYCINE RECEPT (rev)	GGGT	-----T-----	5' UTR
NMDA RECEPTOR	CCCGC	-----	5' UTR
ACH RECEPTOR B2	GCGGC	-----	5' UTR
NEUROFILIMANE-M	GGGT	-----T-----	5' UTR
B-4 TUBULIN	CGCCG	-----	5' UTR
CORT. RELEASING FCTR	GGCGC	-----	5' UTR
CALBINDIN	GCACA	-----	5' UTR
SYNAPTOTAGMIN-4	GTTCT	-----A-----	5' UTR
HES-3	GGCA	-----	5' UTR
SYNAPTOPHYSIN	CGGCG	-----T-----	5' UTR

FIG. 1A

Evolutionary conservation of NRSEs

HUMAN CALBINDIN	AG-----A-----	5' UTR
CHICKEN CALBINDIN	G-----	
RAT CALBINDIN	AG-----	
MOUSE CALBINDIN	AG-----	
HUMAN CRF:	-----	
RAT CRF	-----	
SHEEP CRF	-----T-----	1st Intron
XENOPUS CRF	-----AA-----	
HUMAN NEURONAL NIC ACHR B-2	-----	
RAT NEURONAL NIC ACHR B-2	-----T-----	5' UTR
HUMAN NMDAR (NR1-1)	-----	
RAT NMDAR (NR1-1)	-----AT-----	5' UTR
HUMAN SYNAPSIN I	-----	
RAT SYNAPSIN I	-----T-----	5' UTR

FIG. 1B

NRSEs in non-neuronal genes			
SOM. ACT. FCTR. (rev)	GTCTCT	-----A	CGCAG
NCAM	GCGAT	-----AA	CCTGG
ATRIAL NATRIURETIC PEPTIDE	TAAAC	-----CG-	CGAGG
RAT APRT (rev)	GCTGA	G-----T	TGACC
BOVINE P-450 (rev)	AGTTC	-----G	AGGCT
CANINE DISTEMPER VIRUS (rev)	TGTCT	---C-T-----G---	AGAGT
SHEEP KERATIN	ATGTG	A-----G-	ATGAG
MOUSE SKELETAL ACTIN (rev)	GCTTC	GG-----C-----	GCCAG
T-CELL RECEPTOR BETA	GTACC	G-----A-T-----	TGACA
PIG LACTALBUMIN (rev)	TGTCT	-----G-----T-A	CATTT

5' UTR
1st Intron
3' UTR
Intron
Intron
Coding region
5' Regulatory
3' Regulatory
Coding Region
Coding Region

FIG. 1C

Transcriptional Repression by λ HZ4

Reporter Plasmid	pCMV-HZ4	Percent CAT activity	Fold repression
pCAT3-S36++	0 μ g	100	-
	1	8.3 \pm 0.6	11.4
	4	3.1 \pm 0.3	32
pCAT3	0	100	-
	1	77 \pm 0.8	1.3
	4	67.5 \pm 3.8	1.5

FIG. 2

Figure 1 displays two sequences of 16 grayscale images, labeled 1 through 16, showing the evolution of a liquid meniscus. The left sequence (frames 1-16) shows the initial state with a flat surface and a central disturbance. The right sequence (frames 1-16) shows the final state with a complex, wavy pattern. An arrow points to the first frame of the left panel.

FIG. 3

4 / 19

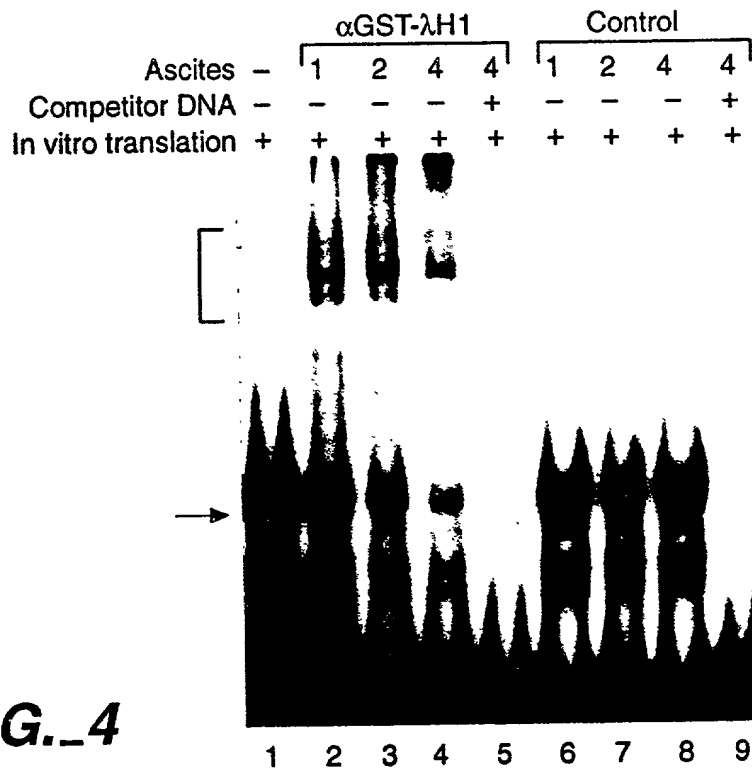
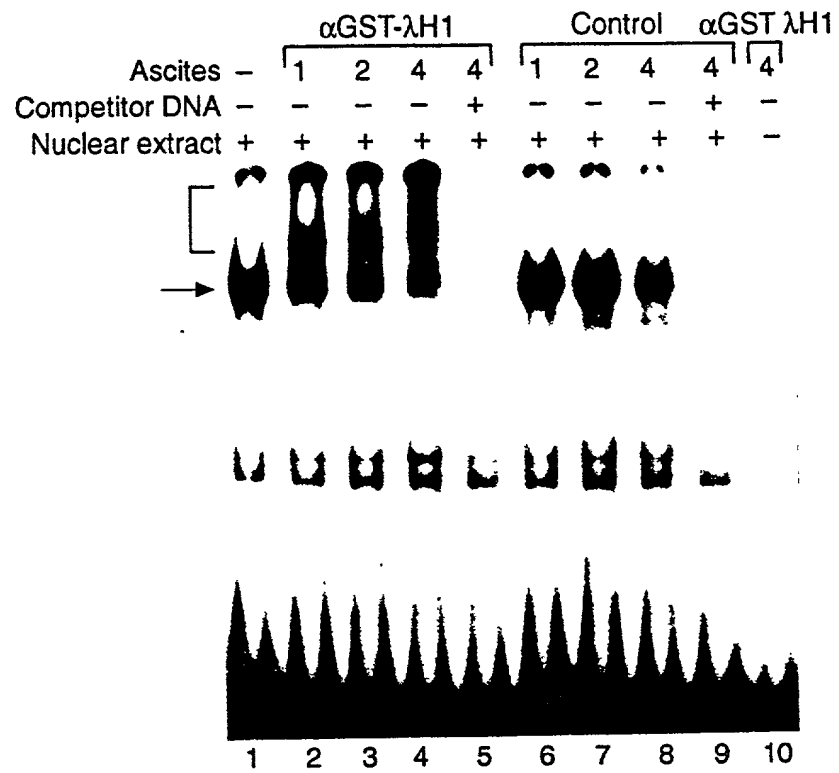


FIG. 4

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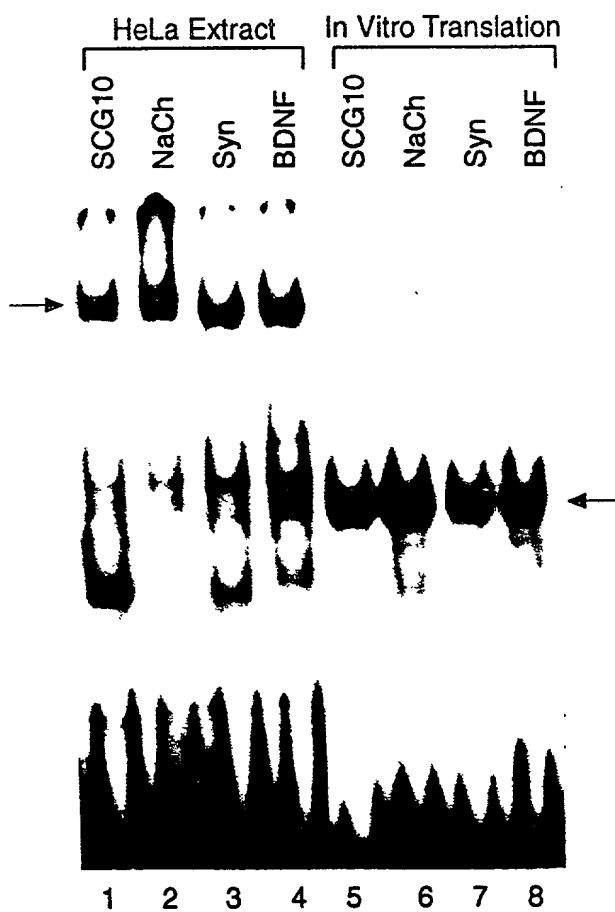


FIG._5

6 / 19

GAATTCC		GGG Gly 1	GCC Ala	CCA Pro	GAC Asp	CCT Pro 5	GGC Gly	GGC Gly	GGC Gly	TGC Cys	GGC Gly 10	AGC Ser	CGA Arg	GAC Asp	GGC Gly	49
AGG Arg 15	GCG Ala	AGG Arg	CCC Pro	GGA Gly	GGC Gly 20	CTG Leu	AGC Ser	ACC Thr	CTC Leu	TGC Cys 25	AGC Ser	CCC Pro	ACT Thr	CCT Pro	GGG Gly 30	97
CCT Pro	TCT Ser	TGG Trp	TCC Ser	ACG Thr 35	ACG Thr	GCC Ala	CCA Pro	GCA Ala	CCC Pro 40	AAC Asn	TTT Phe	ACC Thr	ACC Thr	CTC Leu 45	CCC Pro	145
CAC His	CTC Leu	TCC Ser	CCC Pro 50	GAA Glu	ACT Thr	CCA Pro	GCA Ala	ACA Thr 55	AAG Lys	AAA Lys	AGT Ser	AGT Ser	CGG Arg 60	AGA Arg	AGG Arg	193
AGC Ser	GGC Gly	GAC Asp 65	TCA Ser	GGG Gly	TCG Ser	CCC Pro	GCC Ala 70	CCT Pro	CCT Pro	CAC His	CGA Arg	GGA Gly 75	AGG Arg	CCG Pro	AAT Asn	241
ACA Thr 80	GTT Val	ATG Met	GCC Ala	ACC Thr	CAG Gln	GTA Val 85	ATG Met	GGG Gly	CAG Gln	TCT Ser	TCT Ser 90	GGA Gly	GGA Gly	GGA Gly	GGG Gly	289
CTG Leu 95	TTT Phe	ACC Thr	AGC Ser	AGT Ser	GGC Gly 100	AAC Asn	ATT Ile	GGA Gly	ATG Met	GCC Ala 105	CTG Leu	CCT Pro	AAC Asn	GAC Asp	ATG Met 110	337
TAT Tyr	GAC Asp	TTG Leu	CAT His	GAC Asp 115	CTT Leu	TCC Ser	AAA Lys	GCT Ala	GAA Glu 120	CTG Leu	GCC Ala	GCA Ala	CCT Pro	CAG Gln 125	CTT Leu	385
ATT Ile	ATG Met	CTG Leu	GCA Ala 130	AAT Asn	GTG Val	GCC Ala	TTA Leu	ACT Thr 135	GGG Gly	GAA Glu	GTA Val	AAT Asn	GGC Gly 140	AGC Ser	TGC Cys	433
TGT Cys	GAT Asp	TAC Tyr 145	CTG Leu	GTC Val	GGT Gly	GAA Glu	GAA Glu 150	AGA Arg	CAG Gln	ATG Met	GCA Ala	GAA Glu 155	CTG Leu	ATG Met	CCG Pro	481
GTT Val	GGG Gly 160	GAT Asp	AAC Asn	AAC Asn	TTT Phe	TCA Ser 165	GAT Asp	AGT Ser	GAA Glu	GAA Glu 170	GGA Gly 170	GAA Glu	GGA Gly	CTT Leu	GAA Glu	529
GAG Glu 175	TCT Ser	GCT Ala	GAT Asp	ATA Ile	AAA Lys 180	GGT Gly	GAA Glu	CCT Pro	CAT His	GGA Gly 185	CTG Leu	GAA Glu	AAC Asn	ATG Met	GAA Glu 190	577
CTG Leu	AGA Arg	AGT Ser	TTG Leu	GAA Glu 195	CTC Leu	AGC Ser	GTC Val	GTA Val	GAA Glu 200	CCT Pro	CAG Gln	CCT Pro	GTA Val	TTT Phe 205	GAG Glu	625
GCA Ala	TCA Ser	GGT Gly	GCT Ala 210	CCA Pro	GAT Asp	ATT Ile	TAC Tyr 215	AGT Ser	TCA Ser	AAT Asn	AAA Lys	GAT Asp	CTT Leu 220	CCC Pro	CCT Pro	673
GAA Glu	ACA Thr	CCT Pro 225	GGA Gly	GCG Ala	GAG Glu	GAC Asp	AAA Lys 230	GGC Gly	AAG Lys	AGC Ser	TCG Ser 235	AAG Lys	ACC Thr	AAA Lys	CCC Pro	721

FIG._6A**SUBSTITUTE SHEET (RULE 26)**

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7/19

TTT	CGC	TGT	AAG	CCA	TGC	CAA	TAT	GAA	GCA	GAA	TCT	GAA	GAA	CAG	TTT	769
Phe	Arg	Cys	Lys	Pro	Cys	Gln	Tyr	Glu	Ala	Glu	Ser	Glu	Glu	Gln	Phe	
240						245					250					
GTG	CAT	CAC	ATC	AGA	GTT	CAC	AGT	GCT	AAG	AAA	TTT	TTT	GTG	GAA	GAG	817
Val	His	His	Ile	Arg	Val	His	Ser	Ala	Lys	Lys	Phe	Phe	Val	Glu	Glu	
255					260					265					270	
AGT	GCA	GAG	AAG	CAG	GCA	AAA	GCC	AGG	GAA	TCT	GGC	TCT	TCC	ACT	GCA	865
Ser	Ala	Glu	Lys	Gln	Ala	Lys	Ala	Arg	Glu	Ser	Gly	Ser	Ser	Thr	Ala	
				275					280					285		
GAA	GAG	GGA	GAT	TTC	TCC	AAG	GGC	CCC	ATT	CGC	TGT	GAC	CGC	TGC	GGC	913
Glu	Glu	Gly	Asp	Phe	Ser	Lys	Gly	Pro	Ile	Arg	Cys	Asp	Arg	Cys	Gly	
			290					295					300			
TAC	AAT	ACT	AAT	CGA	TAT	GAT	CAC	TAT	ACA	GCA	CAC	CTG	AAA	CAC	CAC	961
Tyr	Asn	Thr	Asn	Arg	Tyr	Asp	His	Tyr	Thr	Ala	His	Leu	Lys	His	His	
	305						310					315				
ACC	AGA	GCT	GGG	GAT	AAT	GAG	CGA	GTC	TAC	AAG	TGT	ATC	ATT	TGC	ACA	1009
Thr	Arg	Ala	Gly	Asp	Asn	Glu	Arg	Val	Tyr	Lys	Cys	Ile	Ile	Cys	Thr	
	320					325					330					
TAC	ACA	ACA	GTG	AGC	GAG	TAT	CAC	TGG	AGG	AAA	CAT	TTA	AGA	AAC	CAT	1057
Tyr	Thr	Thr	Val	Ser	Glu	Tyr	His	Trp	Arg	Lys	His	Leu	Arg	Asn	His	
335					340					345					350	
TTT	CCA	AGG	AAA	GTA	TAC	ACA	TGT	GGA	AAA	TGC	AAC	TAT	TTT	TCA	GAC	1105
Phe	Pro	Arg	Lys	Val	Tyr	Thr	Cys	Gly	Lys	Cys	Asn	Tyr	Phe	Ser	Asp	
			355					360						365		
AGA	AAA	AAC	AAT	TAT	GTT	CAG	CAT	GTT	AGA	ACT	CAT	ACA	GGA	GAA	CGC	1153
Arg	Lys	Asn	Asn	Tyr	Val	Gln	His	Val	Arg	Thr	His	Thr	Gly	Glu	Arg	
			370				375						380			
CCA	TAT	AAA	TGT	GAA	CTT	TGT	CCT	TAC	TCA	AGT	TCT	CAG	AAG	ACT	CAT	1201
Pro	Tyr	Lys	Cys	Glu	Leu	Cys	Pro	Tyr	Ser	Ser	Ser	Gln	Lys	Thr	His	
		385				390						395				
CTA	ACT	AGA	CAT	ATG	CGT	ACT	CAT	TCA	GGT	GAG	AAG	CCA	TTT	AAA	TGT	1249
Leu	Thr	Arg	His	Met	Arg	Thr	His	Ser	Gly	Glu	Lys	Pro	Phe	Lys	Cys	
	400					405					410					
GAT	CAG	TGC	AGT	TAT	GTG	GCC	TCT	AAT	CAA	CAT	GAA	GTA	ACC	CGC	CAT	1297
Asp	Gln	Cys	Ser	Tyr	Val	Ala	Ser	Asn	Gln	His	Glu	Val	Thr	Arg	His	
415					420					425					430	
GCA	AGA	CAG	GTT	CAC	AAT	GGG	CCT	AAA	CCT	CTT	AAT	TGC	CCA	CAC	TGT	1345
Ala	Arg	Gln	Val	His	Asn	Gly	Pro	Lys	Pro	Leu	Asn	Cys	Pro	His	Cys	
			435					440					445			
GAT	TAC	AAA	ACA	GCA	GAT	AGA	AGC	AAC	TTC	AAA	AAA	CAT	GTA	GAG	CTA	1393
Asp	Tyr	Lys	Thr	Ala	Asp	Arg	Ser	Asn	Phe	Lys	Lys	His	Val	Glu	Leu	
		450						455					460			

FIG. 6B

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8 / 19

CAT	GTG	AAC	CCA	CGG	CAG	TTC	AAT	TGC	CCT	GTA	TGT	GAC	TAT	GCA	GCT	1441
His	Val	Asn	Pro	Arg	Gln	Phe	Asn	Cys	Pro	Val	Cys	Asp	Tyr	Ala	Ala	
		465					470					475				
TCC	AAG	AAG	TGT	AAT	CTA	CAG	TAT	CAC	TTC	AAA	TCT	AAG	CAT	CCT	ACT	1489
Ser	Lys	Lys	Cys	Asn	Leu	Gln	Tyr	His	Phe	Lys	Ser	Lys	His	Pro	Thr	
	480					485					490					
TGT	CCT	AAT	AAA	ACA	ATG	GAT	GTC	TCA	AAA	GTG	AAA	CTA	AAG	AAA	ACC	1537
Cys	Pro	Asn	Lys	Thr	Met	Asp	Val	Ser	Lys	Val	Lys	Leu	Lys	Lys	Thr	
495					500					505					510	
AAA	AAA	CGA	GAG	GCT	GAC	TTG	CCT	GAT	AAT	ATT	ACC	AAT	GAA	AAA	ACA	1585
Lys	Lys	Arg	Glu	Ala	Asp	Leu	Pro	Asp	Asn	Ile	Thr	Asn	Glu	Lys	Thr	
			515						520					525		
GAA	ATA	GAA	CAA	ACA	AAA	ATA	AAA	GGG	GAT	GTG	GCT	GGA	AAG	AAA	AAT	1633
Glu	Ile	Glu	Gln	Thr	Lys	Ile	Lys	Gly	Asp	Val	Ala	Gly	Lys	Lys	Asn	
			530					535					540			
GAA	AAG	TCC	GTC	AAA	GCA	GAG	AAA	AGA	GAT	GTC	TCA	AAA	GAG	AAA	AAG	1681
Glu	Lys	Ser	Val	Lys	Ala	Glu	Lys	Arg	Asp	Val	Ser	Lys	Glu	Lys	Lys	
		545					550					555				
CCT	TCT	AAT	AAT	GTG	TCA	GTG	ATC	CAG	GTG	ACT	ACC	AGA	ACT	CGA	AAA	1729
Pro	Ser	Asn	Asn	Val	Ser	Val	Ile	Gln	Val	Thr	Thr	Arg	Thr	Arg	Lys	
	560					565					570					
TCA	GTA	ACA	GAG	GTG	AAA	GAG	ATG	GAT	GTG	CAT	ACA	GGA	AGC	AAT	TCA	1777
Ser	Val	Thr	Glu	Val	Lys	Glu	Met	Asp	Val	His	Thr	Gly	Ser	Asn	Ser	
575					580					585					590	
GAA	AAA	TTC	AGT	AAA	ACT	AAG	AAA	AGC	AAA	AGG	AAG	CTG	GAA	GTT	GAC	1825
Glu	Lys	Phe	Ser	Lys	Thr	Lys	Lys	Ser	Lys	Arg	Lys	Leu	Glu	Val	Asp	
			595					600						605		
AGC	CAT	TCT	TTA	CAT	GGT	CCT	GTG	AAT	GAT	GAG	GAA	TCT	TCA	ACA	AAA	1873
Ser	His	Ser	Leu	His	Gly	Pro	Val	Asn	Asp	Glu	Glu	Ser	Ser	Thr	Lys	
			610					615				620				
AAG	AAA	AAG	AAG	GTA	GAA	AGC	AAA	TCC	AAA	AAT	AAT	AGT	CAG	GAA	GTG	1921
Lys	Lys	Lys	Lys	Val	Glu	Ser	Lys	Ser	Lys	Asn	Asn	Ser	Gln	Glu	Val	
		625					630					635				
CCA	AAG	GGT	GAC	AGC	AAA	GTG	GAG	GAG	AAT	AAA	AAG	CAA	AAT	ACT	TGC	1969
Pro	Lys	Gly	Asp	Ser	Lys	Val	Glu	Glu	Asn	Lys	Lys	Gln	Asn	Thr	Cys	
	640					645					650					
ATG	AAA	AAA	AGT	ACA	AAG	AAG	AAA	ACT	CTG	AAA	AAT	AAA	TCA	AGT	AAG	2017
Met	Lys	Lys	Ser	Thr	Lys	Lys	Lys	Thr	Leu	Lys	Asn	Lys	Ser	Ser	Lys	
655					660					665					670	
AAA	AGC	AGT	AAG	CCT	TCT	CGGAATTC										2043
Lys	Ser	Ser	Lys	Pro	Ser											
				675												

FIG. 6C
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FIG. 6C
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10 / 19

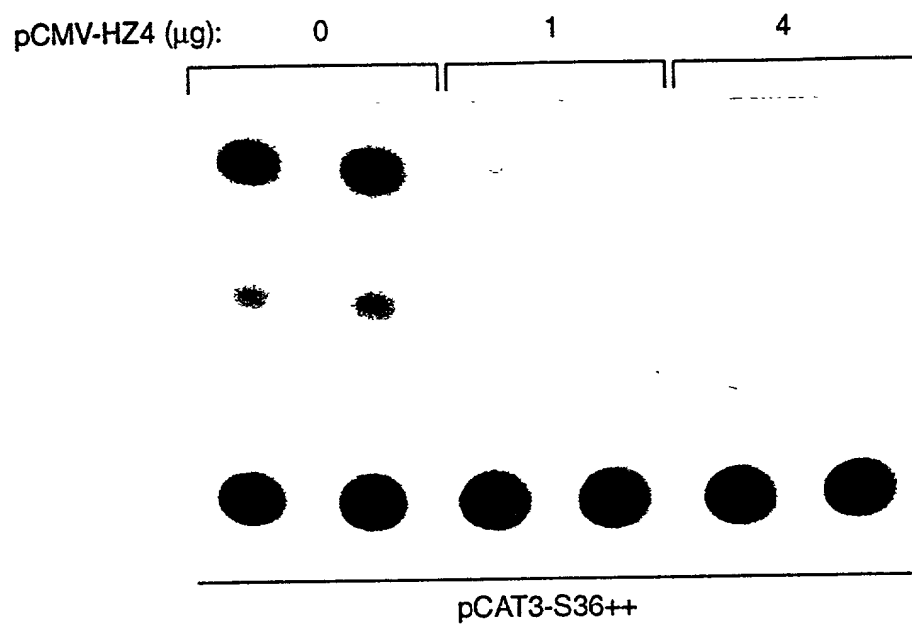


FIG._8A

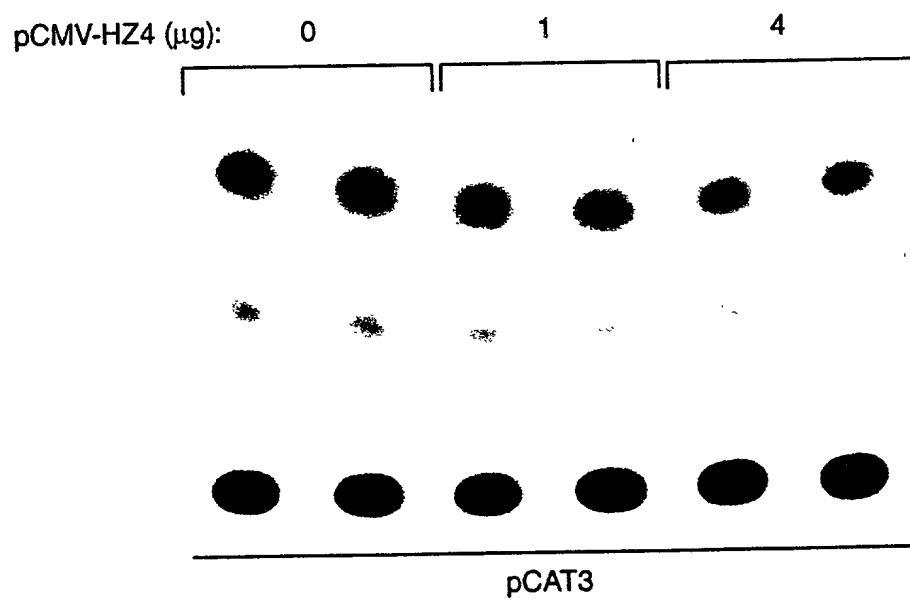


FIG._8B

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11 / 19

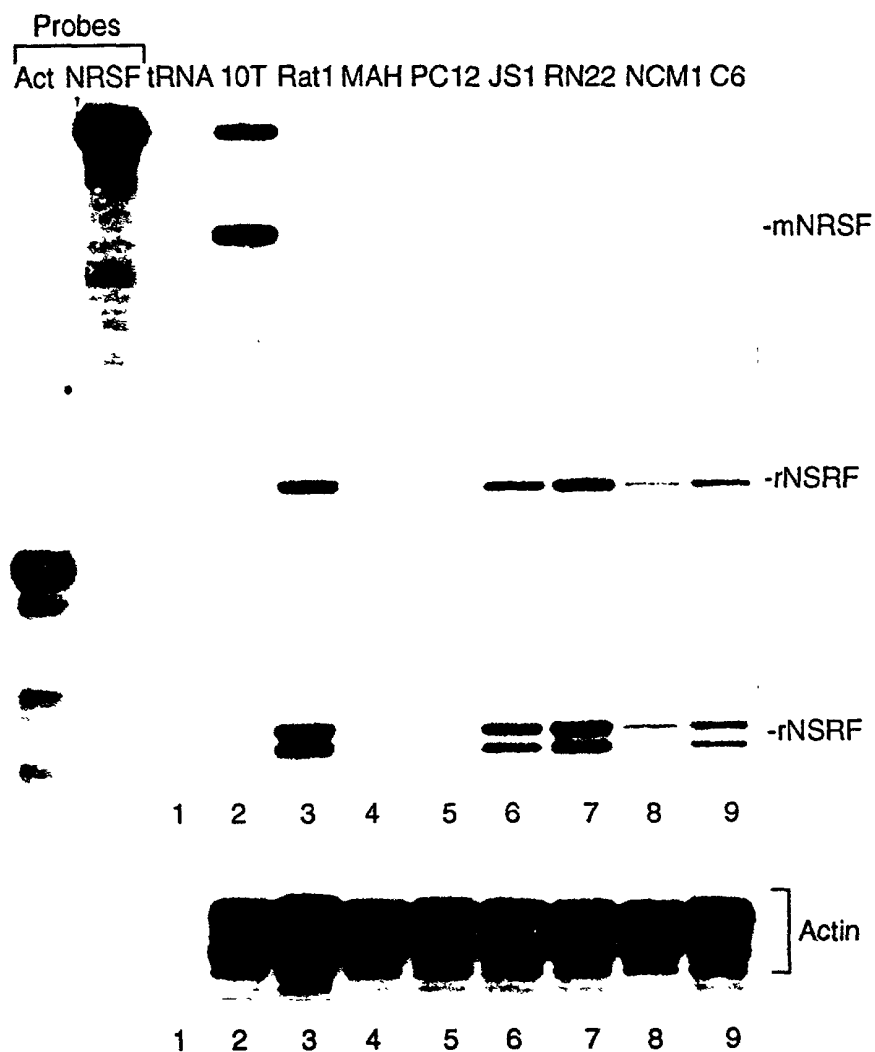


FIG._9



FIG. 10B



FIG. 10A

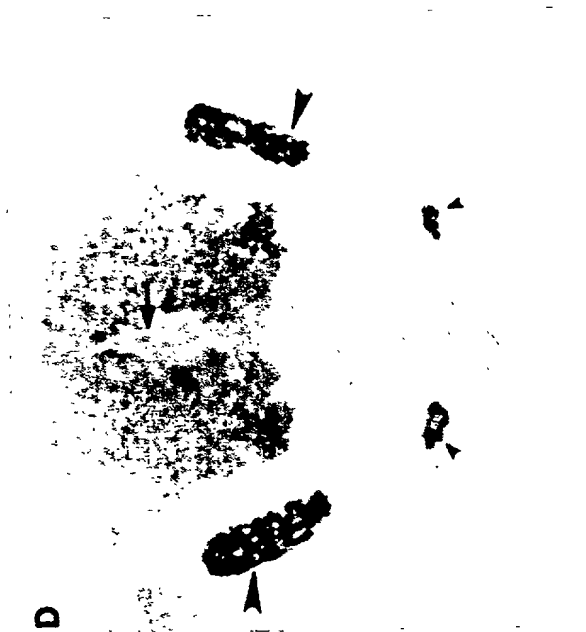


FIG. 10D

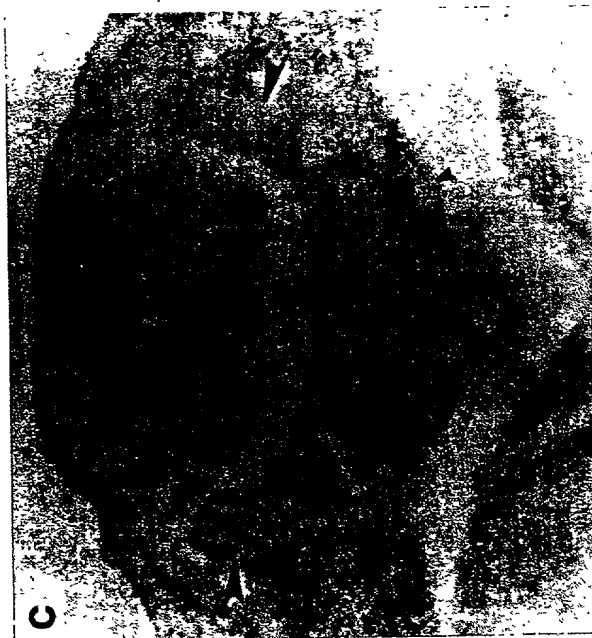


FIG. 10C



FIG. 11C



FIG. 11B



FIG. 11A

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15 / 19

TTCGGACGAG	GCGGGCGGGC	GGCGACGGCG	CGGGCGGGTG	CGCGGCGCAG	CGTCCTGTGC	60
TGGAATGTGC	GGCTCCCGCG	AGCTCGCGGC	GCAGCAGCAG	AAGACCGAGG	AGCGCCGCCG	120
AGGCCGCGGG	CCCCAGACCC	GGGCGGCCGG	GACCGCAGCG	ACGGCAGAAC	CAGGGCCGGC	180
GGTCTGATCC	CGCTCCGCGA	TCGCACCCCG	GGATCTCGAG	GGCCTCGACG	CCCAACTTTT	240
CCCCGCTCTC	CCTCCCCTCC	CCTCCCCCGA	AAGTCCAGCA	ACAAAGAAAA	GGAGTTGGAG	300
CGGCGRCGAC	GCGGGGGTGG	CGGACCGTGG	GCGCACAGTT	CAGAGGAGTA	CAGTT ATG	358
					Met	
					1	
GCC ACC CAG	GTG ATG GGG	CAG TCT TCT	GGA GGA GGC	AGT CTC TTC	AAC	406
Ala Thr Gln	Val Met Gly	Gln Ser Ser	Gly Gly Gly	Ser Leu Phe	Asn	
	5		10		15	
AAC AGT GCC	AAC ATG GGC	ATG GSC	TTA ACC AAC	GAC ATG TAC	GAC CTG	454
Asn Ser Ala	Asn Met Gly	Met Xaa	Leu Thr Asn	Asp Met Tyr	Asp Leu	
	20		25		30	
CAC GAG CTC	TCG AAA GCT	GAA CTG	GCA GCC CCT	CAG CTC ATC	ATG TTA	502
His Glu Leu	Ser Lys Ala	Glu Leu	Ala Ala Pro	Gln Leu Ile	Met Leu	
	35		40		45	
GCC AAC GTG	GCC CTG ACG	GGG GAG	GCA AGC GGC	AGC TGC TGC	GAT TAC	550
Ala Asn Val	Ala Leu Thr	Gly Glu	Ala Ser Gly	Ser Cys Cys	Asp Tyr	
	50		55		60	65
CTG GTC GGT	GAA GAG AGG	CAG ATG GCC	GAA TTG ATG	CCC GTG GGA	GAC	598
Leu Val Gly	Glu Glu Arg	Gln Met Ala	Glu Leu Met	Pro Val Gly	Asp	
	70		75		80	
AAC CAC TTC	TCA GAA AGT	GAA GGA	GAA GGC	CTG GAA GAG	TCG GCT	646
Asn His Phe	Ser Glu Ser	Glu Gly	Glu Gly Leu	Glu Glu Ser	Ala Asp	
	85		90		95	
CTC AAA GGG	CTG GAA AAC	ATG GAA	CTG GGA	AGT TTG	GAG CTA	694
Leu Lys Gly	Leu Glu Asn	Met Glu	Leu Gly Ser	Leu Glu Leu	Ser Ala	
	100		105		110	
GTA GAA CCC	CAG CCC GTA	TTT GAA	GCC TCA	GCT GCC	CCA GAA	742
Val Glu Pro	Gln Pro Val	Phe Glu	Ala Ser Ala	Ala Pro Glu	Ile Tyr	
	115		120		125	
AGC GCC AAT	AAA GAT CCC	GCT CCA	GAA ACA	CCC GTG	GCG GAA	790
Ser Ala Asn	Lys Asp Pro	Ala Ala	Pro Glu Thr	Pro Val Ala	Glu Asp	Lys
	130		135		140	145
TGC AGG AGT	TCT AAG GCC	AAG CCC	TTC CGG	TGT AAG	CCT TGC	838
Cys Arg Ser	Ser Lys Ala	Lys Pro	Phe Arg	Cys Lys	Pro Cys	Gln Tyr
	150		155		160	

FIG. 12A**SUBSTITUTE SHEET (RULE 26)**

FOOTNOTES

16 / 19

GAA GCC GAA TCT GAA GAG CAG TTT GTG CAT CAC ATC CGG ATT CAC AGC Glu Ala Glu Ser Glu Glu Gln Phe Val His His Ile Arg Ile His Ser	886
165 170 175	
GCT AAG AAG TTC TTT GTG GAG GAA AGT GCA GAG AAA CAG GCC AAA GCC Ala Lys Lys Phe Phe Val Glu Glu Ser Ala Glu Lys Gln Ala Lys Ala	934
180 185 190	
TGG GAG TCG GGG TCG TCT CCG GCC GAA GAG GGC GAG TTC TCC AAA GGC Trp Glu Ser Gly Ser Ser Pro Ala Glu Glu Gly Glu Phe Ser Lys Gly	982
195 200 205	
CCC ATC CGC TGT GAC CGC TGT GGC TAC AAT ACC AAC CGG TAT GAC CAC Pro Ile Arg Cys Asp Arg Cys Gly Tyr Asn Thr Asn Arg Tyr Asp His	1030
210 215 220 225	
TAC ATG GCA CAC CTG AAG CAC CAC CTG CGA GCT GGC GAG AAC GAG CGC Tyr Met Ala His Leu Lys His His Leu Arg Ala Gly Glu Asn Glu Arg	1078
230 235 240	
ATC TAC AAG TGC ATC ATC TGC ACG TAC ACG ACG GTC AGC GAG TAC CAC Ile Tyr Lys Cys Ile Ile Cys Thr Thr Thr Val Ser Glu Tyr His	1126
245 250 255	
TGG AGG AAA CAC CTG AGA AAC CAT TTC CCC AGG AAA GTC TAC ACC TGC Trp Arg Lys His Leu Arg Asn His Phe Pro Arg Lys Val Tyr Thr Cys	1174
260 265 270	
AGC AAG TGC AAC TAC TTC TCA GAC AGA AAA AAT AAC TAC GTT CAG CAC Ser Lys Cys Asn Tyr Phe Ser Asp Arg Lys Asn Asn Tyr Val Gln His	1222
275 280 285	
GTG CGA ACT CAC ACA GGA GAA CGC CCG TAT AAA TGT GAA CTT TGT CCT Val Arg Thr His Thr Gly Glu Arg Pro Tyr Lys Cys Glu Leu Cys Pro	1270
290 295 300 305	
TAC TCA AGC TCT CAG AAG ACT CAT CTA ACG CGA CAC ATG CGG ACT CAT Tyr Ser Ser Ser Gln Lys Thr His Leu Thr Arg His Met Arg Thr His	1318
310 315 320	
TCA GGT GAG AAG CCA TTT AAA TGT GAT GAG TGC AAT TAT GTG GCC TCT Ser Gly Glu Lys Pro Phe Lys Cys Asp Glu Cys Asn Tyr Val Ala Ser	1366
325 330 335	
AAT CAG CAT GAA GTG ACC CGA CAT GCA AGA CAG GTT CAC AAC GGG CCT Asn Gln His Glu Val Thr Arg His Ala Arg Gln Val His Asn Gly Pro	1414
340 345 350	
AAA CCT CTT AAT TGC CCG CAC TGT GAC TAC AAA ACA GCA GAT AGA AGC Lys Pro Leu Asn Cys Pro His Cys Asp Tyr Lys Thr Ala Asp Arg Ser	1462
355 360 365	
AAC TTC AAA AAG CAC GTG GAG CTG CAT GTT AAC CCA CGG CAG TTC AAC Asn Phe Lys Lys His Val Glu Leu His Val Asn Pro Arg Gln Phe Asn	1510
370 375 380 385	

FIG. 12B**SUBSTITUTE SHEET (RULE 26)**

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[illegible][illegible][illegible][illegible]

19 / 19

CCC ATG AAA GAC TCC GCA GCA GAG CCA GTG TCC CCT CCT ACC CCA ACA	2902
Pro Met Lys Asp Ser Ala Ala Glu Pro Val Ser Pro Pro Thr Pro Thr	
835 840 845	
GTG GAC CGT GAC GCA GGG TCA CCA GCT GTA GTG GCC TCC CCT CCT ATC	2950
Val Asp Arg Asp Ala Gly Ser Pro Ala Val Val Ala Ser Pro Pro Ile	
850 855 860 865	
ACG TTG GCT GAA AAC GAG TCT CAG GAA ATT GAT GAA GAT GAA GGC ATC	2998
Thr Leu Ala Glu Asn Glu Ser Gln Glu Ile Asp Glu Asp Glu Gly Ile	
870 875 880	
CAT AGC CAT GAT GGA AGT GAC CTG AGT GAC AAC ATG TCT GAG GGG AGT	3046
His Ser His Asp Gly Ser Asp Leu Ser Asp Asn Met Ser Glu Gly Ser	
885 890 895	
GAC GAC TCA GGA CTG CAC GGG GCT CGG CCG ACA CCA CCA GAA GCT ACG	3094
Asp Asp Ser Gly Leu His Gly Ala Arg Pro Thr Pro Pro Glu Ala Thr	
900 905 910	
TCA AAA AAT GGG AAG GCA GGG TTG GCT GGT AAA GTG ACT GAG GGA GAG	3142
Ser Lys Asn Gly Lys Ala Gly Leu Ala Gly Lys Val Thr Glu Gly Glu	
915 920 925	
TTT GTG TGT ATT TTC TGT GAT CGT TCT TTT AGA AAG GAA AAA GAT TAT	3190
Phe Val Cys Ile Phe Cys Asp Arg Ser Phe Arg Lys Glu Lys Asp Tyr	
930 935 940 945	
AGC AAA CAC CTC AAT CGC CAC TTG GTG AAT GTG TAC TTC CTA GAA GAA	3238
Ser Lys His Leu Asn Arg His Leu Val Asn Val Tyr Phe Leu Glu Glu	
950 955 960	
GCA GCT GAG GAG CAG GAG GAG CAG GAG GAG CGG GAG GAG CAG GAG TAG	3286
Ala Ala Glu Glu Gln Glu Glu Gln Glu Glu Arg Glu Glu Gln Glu *	
965 970 975	
CTGAGCCTCG GGAGAAGCAC CGTGCAGACT TTGTGAGCAT GCAATTTTAA TTTGTAGACA	3346
AACGCAAGCT TGCTTTAATT AGTCTCCAAG GCTGAGTTTT CAGTAACATT CTTTTCTTAA	3406
GGACTGTACA TCTATTTAGT GTTTGTGTGCA TAAATCTTAG CAAATCCTCG GGAGTTAATG	3466
TAAGAGGACA GATATGTAAC TAGCTCGTGC AGGCAGGTGC AAGGAGAAGG GTAAGATGGT	3526
GGAACACACC ACTTGCCTTG TCTGCCTACA ACCTGTTGGG TTTTCTTTTC ACGGTAGTTC	3586
CTAATTTTTTA GTTACTTGTT TAGATCGATA AAAATTGGCT TAGTAAATTA CTTGAAGAAT	3646
TTGCCTGCTT TATATAAATT AAGTTAGCAC TTTACAGTTY CTTTAGAGAT GAAAAAAAAG	3706
AGATTTTAAT TGGAGAGAAA TTCTCAACAT TGGACATTGT ATCTGTCCAG GTAATTGCTT	3766
CCTAACTTGC TATCAATATT TTGTGTTTAT ATGTTAATCG TTATAAAAAG TGATTTTTGT	3826
TTTTTGGGTA TTTTTTATTT TGGTGCTTTT CTGGCTTAAG ATGTTGCACA TGGTCTTGT	3886
TTTTGTTTCT TTAACCTATG CAGTTAATCT CCCTTCCCT GAAACAGCGT TGTGTTAAAT	3946
AGTAACACTA TACAGATATA TGCATGGTTT TTTTTTTTGT TTGTTTGTGT GTTTGTTTTT	4006
CCTTTTTTGA GGGATGCTTT TAGGCTTGTT TGCCTCGTSC CGAATTCGAT A	4057

FIG. 12E
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FIG. 12E